

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2001, 10:54:58 ; Search time 7124.02 Seconds
(without alignments)
11995.940 Million cell updates/sec

Title: US-09-515-806-1

Perfect score: 5525

Sequence: 1 tcgcccacggtccgcacc.....aatgtttcatataacctgca 5525

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba1.*

2: gb_ba2.*

3: gb_ba3.*

4: gb_in1.*

5: gb_in2.*

6: gb_in3.*

7: gb_om.*

8: gb_ov.*

9: gb_pat1.*

10: gb_pat2.*

11: gb_ph.*

12: gb_pl1.*

13: gb_pl2.*

14: gb_pl3.*

15: gb_pl4.*

16: em_ba1.*

17: em_ba2.*

18: em_fun.*

19: em_htgo_hum.*

20: em_htgo_inv.*

21: em_htgo_rod.*

22: em_htg_hum1.*

23: em_htg_hum2.*

24: em_htg_hum3.*

25: em_htg_hum4.*

26: em_htg_hum5.*

27: em_htg_hum6.*

28: em_htg_hum7.*

29: em_htg_hum8.*

30: em_htg_inv1.*

31: em_htg_inv2.*

32: em_htg_other.*

33: em_htg_rod.*

34: em_hum1.*

35: em_hum2.*

36: em_hum3.*

37: em_hum4.*

38: em_hum5.*

39: em_hum6.*

40: em_hum7.*

41: em_in.*

42: em_om.*

43: em_or.*

44: em_ov.*
45: em_pat.*
46: em_ph.*
47: em_pl.*
48: em_ro.*
49: em_sts.*
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52: em_vi.*
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54: gb_sts2.*
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56: gb_sy.*
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91: gb_pr7.*
92: gb_pr8.*
93: gb_pr9.*
94: gb_rol.*
95: gb_rol2.*
96: gb_in4.*
97: gb_pr10.*
98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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Db	717	gctgcattgctggggccgtggggccccggcgccggcgagcagccctccggagagc	836
QY	777	gctgcattgctggggccgtggggccccggcgccggcgagcagccctccggagagc	858
Db	777	gctgcattgctggggccgtggggccccggcgccggcgagcagccctccggagagc	896
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QY	1017	gctgcattgctggggccgtggggccccggcgccggcgagcagccctccggagagc	1095
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[illegible]

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Db	4093	AGGCAGAGGGTGTGCGCTGAGATCTTTCAGCTGTGTGGCAGATATGACTGCTGATTCCC	4152
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Db	4213	ATAGACAAGATATTTGCGCGCTGTCTCAACATGGGAGAGCCCTGTTACAGTGTGAGCTCTGT	4272
QY	4254	gacctctgttgttaagttgttgtagtctatgtccagggccatcaacctaaacccag	4313
Db	4273	GACCTCTGTTGTACGTGCTGGCCAGATGTCCATGTCCAGGGCCATCAACCTTAACCCAG	4332
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Db	4333	AAACTCTGGACGGCGGCATCTACTGCAGAGATCATGTATGACTGGTGCACAGTCCCGAGAA	4392
QY	4374	gaattacaagtaactgcagacaataatgaatacactatgtggcccttgtctoggtataaa	4433
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Db	3185	GCAGATGGAGAAATCCGAGCTGCATGAAGTCTGCACACACAGCTGGCCACACGGATGG	3244
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AF193342 5141 bp mRNA ROD 11-OCT-2000
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DEFINITION AF193342
VERSION AF193342.1 GI:10764160
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SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5141)
AUTHORS Sood, R., Porter, A.C., Olsen, D.A., Cavenier, D.R. and Wek, R.C.
TITLE A mammalian homologue of GCN2 protein kinase important for
translational control by phosphorylation of eukaryotic initiation
factor-2alpha
JOURNAL Genetics 154 (2), 787-801 (2000)
MEDLINE 20157056
PUBMED 10655230
REFERENCE 2 (bases 1 to 5141)
AUTHORS Sood, R., Porter, A.C., Olsen, D.A., Cavenier, D.R. and Wek, R.C.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1999) Biochemistry and Molecular Biology, Indiana
University School of Medicine, MS 4067, 635 Barnhill Drive,
Indianapolis, IN 46202, USA
FEATURES
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Matches 3835; Conservative 0; Mismatches 611; Indels 10; Gaps 4;
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Query Match	60.3%	Score 3332	DB 93	Length 3351	
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QY 2794	aggtccaaagaaagcacaac	2853			
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 ACCESSION AJ243428
 VERSION AJ243428.1 GI:6065913

KEYWORDS eIF2 alpha kinase; GCN2 gene.
 SOURCE human.
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 REFERENCE 1 (bases 1 to 2162)
 AUTHORS Berlanga, J., Santoyo, J. and De Haro, C.
 TITLE Characterization of a mammalian homolog of the GCN2 eukaryotic initiation factor 2alpha kinase
 JOURNAL Eur. J. Biochem. 265 (2), 754-762 (1999)
 MEDLINE 99435990
 REFERENCE 2 (bases 1 to 2162)
 AUTHORS Santoyo, J.
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 JOURNAL Submitted (28-JUN-1999) Santoyo J., Molecular Biology, Centro de Biología Molecular 'Severo Ochoa', Fac. Ciencias. U.A.M., Cantoblanco, Madrid, 28049, SPAIN
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DEFINITION			
ACCESSION			
VERSION			
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LOCUS Homo sapiens mRNA; cDNA DKFp434H149 (from clone DKFp434H149).			
ACCESSION AL137676			
VERSION AL137676.1 GI:6807846			

RESULT 10

RESOLVED TO
HCSM802022

MODULO 1

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

REFERENCES

German Genome Project.
This clone (DRF2p43H149) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

FEATURES

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/db_xref="taxon:9606"
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Matches 1903; Conservative 0; Mismatches 4; Indels 183; Gaps 3;

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DEFINITION partial cds.
ACCESSION AL137627
VERSION AL137627.1 GI:6808424
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1138)
Duesternhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
Direct Submission
Submitted (15-JAN-2000) MIPS, Am Klopferspitze 18a, D-82152
Martinsried, GERMANY
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Oligen (Hilden/Germany) within the CDNA sequencing
consortium of the German Genome Project.
This clone (DKF2p434P0612) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
Location/Qualifiers
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polyA_site 1078
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Db 961 AAAAAAAAAAAAAAAAAAATTTTTTTCTAAGAGCTGCTCCACAAAGTTGAGCTTTGT 1020
Qy 5457 tagttttcatgtgtaataattataaattattcttttgggataataaattgcttcat 5516
|||||
Db 1021 TAGTTTTTCATGTATATATATAAATTTACTTTTGGGATATATAAATGCTTTCAT 1080
Qy 5517 ata 5519
|||
Db 1081 ATA 1083

RESULT 12
AC021755
LOCUS
DEFINITION Homo sapiens chromosome 15 clone RP11-521C20 map 15q14, WORKING
DRAFT SEQUENCE, 6 ordered pieces.
ACCESSION AC021755
VERSION AC021755.6 GI:13399357
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157900)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A.,
Nesbitt,R., Traicoff,R. and Hood,L.
Sequencing of human chromosome 15 D15S146-D15S117 region
Unpublished
2 (bases 1 to 157900)
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
and Hood,L.
Direct Submission
Submitted (20-JAN-2000) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
On Mar 21, 2001 this sequence version replaced gi:8272664.

Genome Center
Center: Multimegabase Sequencing Center
Web site: <http://chroma.mbt.washington.edu/msg.www>
Contact: leetowen@systemsbiology.org

Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
Insert size: 150000; agarose-1p
Quality coverage: 10.2x in Q20 bases; sum-of-contigs

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 67961: contig of 67961 bp in length
* 67962 68061: gap of unknown length
* 68062 76767: contig of 8706 bp in length

FEATURES
Source
1..157900
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15q14"
/clone="RP11-521C20"
/clone_lib="rPCI human BAC library 11"
/note="This clone overlaps RP11-43D14 and CTD-2006D8"
BASE COUNT 43137 a 35607 c 36148 g 42500 t 508 others
ORIGIN

Query Match 10.3%; Score 568.8; DB 66; Length 157900;
Best Local Similarity 99.7%; Pred. No. 1.8e-103;
Matches 570; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4953 aaggtgtctgtctatttctgtacagctatagatgactactacagaattcttatttaa 5012
|||||
Db 52724 AGGGTGTCTGTCTATTCTGTACAGCTATAGAGTACTACTACAGAATCTTATTAA 52783
Qy 5013 ccctaaagaactgtcttaacctcattcaaacagacagagagcttactggaataatgga 5072
|||||
Db 52784 CCTAAAGAACTCGTGTAACTCATTTCAACACAGACAGAGGCTTATATCGGAATATGGA 52843
Qy 5073 atgtgtacattcatcaatttaaaatttaattcttaagaagagctgggtgcagtgct 5132
|||||
Db 52844 ATGTTGTACATTCATCATTAATTTAAATTTAAATTTCTTAAGAAGAGGCTGGTGCAGTGGCT 52903
Qy 5133 cacaccttaatccagcacctttgggaagccaagcgaggaagactgcttgaaccaggag 5192
|||||
Db 52904 CACACCTTTAATCCAGCACCTTTGGGAAGCCAGGAGGAGACTGCTTGAACACGAGAG 52963
Qy 5193 ttgagacaccgctgagcaacaagaagaccatctctataaaaaactaaaaaattag 5252
|||||
Db 52964 TTTGAGACAGCCTGAGCAACAAAGCAAGACCCCATCTCTATAAAAACTAAAAAATAG 53023
Qy 5253 ttgggcatgtggtgacatgctgtagtcacagctactccagagctgagatggatcatct 5312
|||||
Db 53024 TTGGCATGTGTGGCACATGCTGTAGTCCCGACCTACTCCAGAGGCTGAGATGGATCATCT 53083
Qy 5313 gagctcaggaggttgaggtgagctgagctgagctgctgactgcgcactgcactccagctggg 5372
|||||
Db 53084 GAGCCTCAGGAGGTTGAGGCTGCAGTGAGCTGCTGACTGCGCCACTGCACCTCCAGCTGGG 53143
Qy 5373 acaacagagaagaccctgtcttaaaaaaagaaaaaatttttttctcaagaag 5432
|||||
Db 53144 ACAACAGAGCAGACCCCTGTCTTAAAAAAGAAAAAATTTTCTTCTAAAGAG 53203
Qy 5433 ctgtcctacaagttgagctttgttagtttttctatgtgtaatatattataattatctt 5492
|||||
Db 53204 CTGTCTCAACAAGTTGAGCTTTGTTAGTTTTCATGTGTATATATATATATATCTT 53263
Qy 5493 ttgggataataaattgctttcatataacctgc 5524
|||||
Db 53264 TTGGGATATAATAAATGCTTTTCATATACCTGC 53295

RESULT 13
AC025168/c
LOCUS AC025168 173364 bp DNA HTG 13-APR-2001
DEFINITION Homo sapiens chromosome 15 clone RP11-43D14 map 15q14, ***
SEQUENCING IN PROGRESS ***, 1 ordered pieces.
ACCESSION AC025168
VERSION AC025168.6 GI:13621223

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L3086
Center clone name: 10_K15

Summary Statistics
Sequencing vector: M13; M7815; 98% of reads
Sequencing vector: Plasmid; n/a; 0.0% of reads
1.91489361702128Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 142640 bases at least Q40

Consensus quality: 152432 bases at least Q30

Consensus quality: 157096 bases at least Q20

Insert size: 153000; agarose-fp

Quality coverage: 3.4 in Q20 bases; agarose-fp

Quality cov.

NOTE: This is a 'working draft' sequence. It currently

consists of 34 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence.

as soon as it is available and the accession number will

be preserved.

1 1064: contig of 1064 bp in length

1065 1164: gap of 100 bp

1165 2366: contig of 1202 bp in length

2367 2466: gap of 100 bp

2467 3540: contig of 1074 bp in length

3541 3640: gap of 100 bp

3641 4861: contig of 1221 bp in length

4862 4961: gap of 100 bp

4962 5968: contig of 1007 bp in length

5969 6068: gap of 100 bp

6069 7242: contig of 1174 bp in length

7243 7342: gap of 100 bp

7343 8433: contig of 1111 bp in length

8434 8553: gap of 100 bp

8554 9820: contig of 1267 bp in length

9821 9920: gap of 100 bp

9921 10938: contig of 1018 bp in length

10939 11038: gap of 100 bp

11039 12256: contig of 1218 bp in length

12257 12356: gap of 100 bp

12357 14248: contig of 1892 bp in length

14249 14348: gap of 100 bp

14349 15680: contig of 1332 bp in length

15681 15780: gap of 100 bp

15781 17240: contig of 1460 bp in length

17241 17340: gap of 100 bp

17341 18693: contig of 1353 bp in length

18694 18793: gap of 100 bp

18794 20812: contig of 2019 bp in length

20813 20912: gap of 100 bp

20913 24906: contig of 3994 bp in length

24907 25006: gap of 100 bp

25007 28926: contig of 3920 bp in length

28927 29026: gap of 100 bp

29027 34159: contig of 5133 bp in length

34160 34259: gap of 100 bp

34260 37975: contig of 3716 bp in length

37976 38075: gap of 100 bp

38076 43955: contig of 5880 bp in length

43956 44055: gap of 100 bp

44056 48039: contig of 3984 bp in length

* 48040 48139: gap of 100 bp
* 48140 53767: contig of 5628 bp in length
* 53768 53967: gap of 100 bp
* 53968 59812: contig of 5945 bp in length
* 59813 59912: gap of 100 bp
* 59913 63066: contig of 3154 bp in length
* 63067 63166: gap of 100 bp
* 63167 70627: contig of 7461 bp in length
* 70628 70727: gap of 100 bp
* 70728 77701: contig of 6974 bp in length
* 77702 77801: gap of 100 bp
* 77802 85553: contig of 7752 bp in length
* 85554 85653: gap of 100 bp
* 85654 94602: contig of 8949 bp in length
* 94603 94702: gap of 100 bp
* 94703 104093: contig of 9391 bp in length
* 104094 104193: gap of 100 bp
* 104194 112395: contig of 8202 bp in length
* 112396 112495: gap of 100 bp
* 112496 123244: contig of 10749 bp in length
* 123245 123344: gap of 100 bp
* 123345 135427: contig of 12083 bp in length
* 135428 135527: gap of 100 bp
* 135528 147434: contig of 11907 bp in length
* 147435 147534: gap of 100 bp
* 147535 164297: contig of 16763 bp in length.

FEATURES

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1. 164297
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-10K15"
/clone_lib="RPC1-11 Human Male BAC"

misc_feature

1165..2366
/note="assembly_fragment"

misc_feature

2467..3540
/note="assembly_fragment"

misc_feature

3641..4861
/note="assembly_fragment"

misc_feature

4962..5968
/note="assembly_fragment"

misc_feature

6069..7242
/note="assembly_fragment"

misc_feature

7343..8453
/note="assembly_fragment"

misc_feature

8554..9820
/note="assembly_fragment"

misc_feature

9921..10938
/note="assembly_fragment"

misc_feature

11039..12256
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misc_feature

12357..14248
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misc_feature

14349..15680
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misc_feature

15781..17240
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misc_feature

17341..18693
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misc_feature

18794..20812
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misc_feature

20913..24906
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misc_feature

25007..28926
/note="assembly_fragment"

misc_feature

29027..34159
/note="assembly_fragment"

misc_feature

34260..37975
/note="assembly_fragment"

clone_end:T7
vector_side:left"

misc_feature

38076..43955

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/note="assembly_fragment"
misc_feature 44056..48039
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misc_feature 48140..53767
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misc_feature 53868..59812
/note="assembly_fragment"
misc_feature 59913..63066
/note="assembly_fragment"
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vector_side:left"
63167..70627
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misc_feature 70728..77701
/note="assembly_fragment"
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/note="assembly_fragment"
misc_feature 85654..94602
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misc_feature 94703..104093
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Query Match 9.8%; Score 542.8; DB 62; Length 164297;

Best Local Similarity 98.7%; Pred. No. 2.6e-98;

Matches 547; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1075 agcagattcaaggaacagaaacagaaattcaactcactgtgtaaaattgagccatcaaatg 1134
|||||
DB 60671 ATCAGATTACAGGAACAGAAACAGAAATTCACCTACTCGTAAATGAGCCATCAAAATG 60612
|||||
QY 1135 tagtcgctaccttgcattgaatcgaagcagagagactccatcgtgtgacattt 1194
|||||
DB 60611 TAGTAGCTACCTTCATGATGATCTCAAGAGCAGAGACTCCATCGTGTGACATTT 60552
|||||
QY 1195 tagtgagacattagtgggtctcttctgtgtgcacactgagccactcagcccatcc 1254
|||||
DB 60551 TAGTGAGCACATTAGTGGGGTCTCTCTGTGTCACACCTGAGCCACTCAGGCCCATCC 60492
|||||
QY 1255 ctgtgcatcagcttcgaggttacacagctcagctcgttcgagccttgatttatcgaca 1314
|||||
DB 60491 CTGTGTCATCAGCTTCGACAGGTACACAGCTCAGCTCTGTCAGGCTTGATTTATCTGCACA 60432
|||||
QY 1315 gcaattctgtgtgataaggtccctgagtcattctaatgtcttgggtgagtcagaaagca 1374
|||||
DB 60431 GCAATTCTGTGTGATAGGTCTCTGAGTGATCTAATGTCTTGGTGGATGCACAAGGCA 60372
|||||
QY 1375 ccgtcaagattacgagactatagcatttctaagcgctcgcagacatttgcaggaggatg 1434
|||||
DB 60371 CCGTCAAGATTACGACTATAGCATTTCTAAGCGCTCGCAGACATTTGCAAGGAGGATG 60312
|||||
QY 1435 tgtttgacaaaccgagttcgcttttagtgcaatgctctccttataaaacggggaaga 1494
|||||
DB 60311 TGTTTTCAGCAAAACCGAGTTGCTTTTGTAGTGAATGCTCTGCTTATATAAACGGGGAGA 60252
|||||
QY 1495 aaggagattgttgctgtctgtcctcctcagcagacagacagaaatgtg 1554
|||||
DB 60251 AAGGAGATGTTGGCGCTCTTGCCCTTCGCTGCTCCTCCTCAGCAAGACAGAAATGTG 60192
|||||
QY 1555 gagagttaccctgtgaccatccctagctactaccagctgactttcaagattttctaaaga 1614
|||||
DB 60191 GAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAACAGATTTTCTAAAGA 60132
|||||
QY 1615 aatgtgtgtgttg 1628
|||||
DB 60131 ACTGAGTATCACTG 60118
|||||

```

RESULT 15

AC090997

LOCUS AC090997 61029 bp DNA

DEFINITION Homo sapiens chromosome 15 clone RP11-521C20 map 15, LOW-PASS

SEQUENCE SAMPLING.

AC090997

VERSION
KEYWORDS
SOURCE
ORGANISM

AC090997.1 GI:13431057

HTG; HTGS_PHASE0.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 61029)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-521C20

Unpublished

2 (bases 1 to 61029)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A.,
Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M.,
Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K.,
Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,
Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K.,
Lamazares, R., Landers, T., Lehotzky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S.,
Severy, P., Sougne, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (22-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L13141

Center clone name: 521_C_20

* NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

```

1 570: contig of 570 bp in length
* 571 670: gap of 100 bp
* 671 1297: contig of 627 bp in length
* 1298 1397: gap of 100 bp
* 1398 2087: contig of 690 bp in length
* 2088 2187: gap of 100 bp
* 2188 2956: contig of 769 bp in length
* 2957 3056: gap of 100 bp
* 3057 3690: contig of 634 bp in length
* 3691 3790: gap of 100 bp
* 3791 4405: contig of 615 bp in length
* 4406 4505: gap of 100 bp
* 4506 5161: contig of 656 bp in length
* 5162 5261: gap of 100 bp
* 5262 5867: contig of 606 bp in length

```


Db 48029 ACCTGAGCAACAAAGCAGACCCCATCTCTATAAACTAAAAAATTANTTGGCATG 48088
QY 5262 gtggcacatgctgtagtccagctactccagagctgagatgagatcatctgagcctcag 5321
|||||
Db 48089 GTGGCACATGCTGTAGTCCAGCTACTCCAGAGGCTGAGATGGATCATCTGAGCCTCAG 48148
QY 5322 gaggttgaggtgcagtgagctgtgactgcgccactgcactccagctctgggacacacagag 5381
|||||
Db 48149 GAGGTTGAGGCTGCAGTGAGCTGTGACTGCGCCACTGCCACTCCAGCTCGGGACACACAGAG 48208
QY 5382 caagaccctgtcttaaaaaaagaaagaaaaatTTTTTcttaagaagctgtccctac 5441
|||||
Db 48209 CAAGACCCTGTCTTAAAAAAGAAAGAAAAAATTTTTTCTAAGAGCTGTCCTAC 48268
QY 5442 aaagttgagctttgttagtttttcag 5468
|||||
Db 48269 AAAAGTTGAGCTTTGTAGTTTTCATG 48295

Search completed: October 21, 2001, 18:18:05
Job time: 26587 sec

